IN THE SPECIFICATION:

Please replace the paragraph beginning at page 7, line 9, with the following rewritten paragraph:

B1 Figure 16 shows the sequence of TaHo-1 (SEQ ID NO:3) and TaHo-2 (positions 1-338 of SEQ ID NO:4). The figure further identifies the E and F residues that are substituted and the amino acid sequences that are deleted in TaHo protein variants set forth (SEQ ID NOS:8-10). Also indicated are the amino acid sequences comprising ankyrin repeats, the SAM domain, and the PARP domain.

Please replace the paragraph beginning at page 12, line 16, with the following rewritten paragraph:

B2 In a preferred embodiment, dominant negative TaHo protein isoforms are provided. Included and preferred among such TaHo proteins are proteins having mutations in an NAD+ binding site. More preferred among these proteins are those with F→L, or E→A, or F→L and E→A mutations in an NAD+ binding site, as those depicted in Figures 5 and 16 (SEQ ID NOS:8-10). Also preferred are TaHo proteins with deletions in the PARP domain at the C-terminus, preferably from amino acids 961-976, or amino acids 430-476, as set forth in Figure 16. Also highly preferred is a TaHo protein with such a C-terminus deletion from amino acids 961-976 as set forth in Figure 16, and having an E→A mutation or an F→L mutation or F→L and E→A mutations.

Please replace the paragraph beginning at page 39, line 6, with the following rewritten paragraph:

B3 Particularly preferred among such dominant negative cell cycle proteins are dominant negative TaHo proteins having mutations in an NAD+ binding site. More preferred among these proteins are those with F→L, E→A, or F→L and E→A amino acid substitutions

in an NAD+ binding site, as those depicted in Figure 5. Also preferred are TaHo proteins with deletions in the PARP domain, preferably from amino acids 461-476 or 430-476 as depicted in Figure 16 (SEQ ID NOS:8-10). Also preferred is a TaHo protein with such a C-terminus deletion from amino acids 461-476 as set forth in Figure 16 and having an F→L, E→A, or F→L and E→A amino acid substitution in an NAD+ binding site, as depicted in Figure 16.

B3 Cont

Please replace the paragraph beginning at page 44, line 36, with the following rewritten paragraph:

A number of cyclin destruction boxes are known in the art, for example, cyclin A has a destruction box comprising the sequence RTVLGVIGD (SEQ ID NO:11); the destruction box of cyclin B1 comprises the sequence RTALGDIGN (SEQ ID NO:12). See Glotzer et al., Nature 349:132-138 (1991). Other destruction boxes are known as well:

B4

YMTVSIIDRFMQDSCVPKKMLQLVGVT (rat cyclin B; SEQ ID NO:13);
KFRLLQETMYMTVSIIDRFMQNSCVPKK (mouse cyclin B; SEQ ID NO:14);
RAILIDWLIQVQMKFRLLQETMYMTVS (mouse cyclin B1; SEQ ID NO:15);
DRFLQAQLVCRKKLQVVGITALLLASK (mouse cyclin B2; SEQ ID NO:16); and
MSVLRGKLQLVGTAAMLL (mouse cyclin A2; SEQ ID NO:17).

On page 63, immediately preceding the heading "CLAIMS," please delete the previously submitted sequence listing and insert there for the enclosed text entitled "SEQUENCE LISTING".

In the Figures:

Please replace Figure 3 with the enclosed replacement formal drawing for Figure 3.